



SEQUENCE LISTING

<110> NAKAJIMA, Hiroaki
NAGASAWA, Akitsu

<120> Method for giving resistance to weed control compounds to plants

<130> 0020-4764P

<140> 09/697,719

<141> 2000-10-27

<150> JP 10/120553

<151> 1998-04-30

<150> JP 10/281127

<151> 1998-10-02

<150> JP 10/330981

<151> 1998-11-20

<150> JP 11/054730

<151> 1999-03-02

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<223> Designed oligonucleotide primer to amplify bchH gene

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<223> Designed oligonucleotide primer to amplify bchH gene

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acggaagctt agatcttcac tcggcggcaa t 31

<210> 3

<211> 39

<212> DNA

<213> Artificial Sequence

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<223> Designed oligonucleotide primer to amplify soybean PPO gene

<400> 3

tcgagctcca tggttccgt cttcaacgag atcctattc 39
 <210> 4
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 Met Val Ser Val Phe Asn Glu Ile Leu Phe Pro Pro Asn Gln Thr Leu
 1 5 10 15
 ctt cgc ccc tcc ctc cat tcc cca acc tct ttc acc tct ccc act 96
 Leu Arg Pro Ser Leu His Ser Pro Thr Ser Phe Phe Thr Ser Pro Thr
 20 25 30
 cga aaa ttc cct cgc tct cgc cct aac cct att cta cgc tgc tcc att 144
 Arg Lys Phe Pro Arg Ser Arg Pro Asn Pro Ile Leu Arg Cys Ser Ile
 35 40 45
 gcg gag gaa tcc acc gcg tct ccg ccc aaa acc aga gac tcc gcc ccc 192
 Ala Glu Glu Ser Thr Ala Ser Pro Pro Lys Thr Arg Asp Ser Ala Pro
 50 55 60
 gtg gac tgc gtc gtc ggc gga ggc gtc agc ggc ctc tgc atc gcc 240
 Val Asp Cys Val Val Gly Gly Val Ser Gly Leu Cys Ile Ala
 65 70 75 80
 cag gcc ctc gcc acc aaa cac gcc aat gcc aac gtc gtc gtc acg gag 288
 Gln Ala Leu Ala Thr Lys His Ala Asn Ala Asn Val Val Thr Glu
 85 90 95
 gcc cga gac cgc gtc ggc ggc aac atc acc acg atg gag agg gac gga 336
 Ala Arg Asp Arg Val Gly Gly Asn Ile Thr Thr Met Glu Arg Asp Gly
 100 105 110
 tac ctc tgg gaa gaa ggc ccc aac agc ttc cag cct tct gat cca atg 384
 Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met
 115 120 125
 ctc acc atg gtg gtc gac agt ggt tta aag gat gag ctt gtt ttg ggg 432
 Leu Thr Met Val Val Asp Ser Gly Leu Lys Asp Glu Leu Val Leu Gly
 130 135 140
 gat cct gat gca cct cgg ttt gtg ttg tgg aac agg aag ttg agg ccg 480
 Asp Pro Asp Ala Pro Arg Phe Val Leu Trp Asn Arg Lys Leu Arg Pro
 145 150 155 160
 gtg ccc ggg aag ctg act gat ttg cct ttc gac ttg atg agc att 528
 Val Pro Gly Lys Leu Thr Asp Leu Pro Phe Phe Asp Leu Met Ser Ile
 165 170 175
 ggt ggc aaa atc agg gct ggc ttt ggt gcg ctt gga att cgg cct cct 576

Gly	Gly	Lys	Ile	Arg	Ala	Gly	Phe	Gly	Ala	Leu	Gly	Ile	Arg	Pro	Pro
180						185					190				
cct	cca	ggg	cat	gag	gaa	tgc	gtt	gaa	gag	ttt	gtt	cgt	cgg	aac	ctt
Pro	Pro	Gly	His	Glu	Glu	Ser	Val	Glu	Glu	Phe	Val	Arg	Arg	Asn	Leu
195						200					205				
ggt	gat	gag	gtt	ttt	gaa	cgg	ttg	ata	gag	cct	ttt	tgt	tca	ggg	gtc
Gly	Asp	Glu	Val	Phe	Glu	Arg	Ile	Glu	Pro	Phe	Cys	Ser	Gly	Val	
210						215					220				
tat	gca	ggc	gat	cct	tca	aaa	tta	agt	atg	aaa	gca	gca	tcc	ggg	aaa
Tyr	Ala	Gly	Asp	Pro	Ser	Lys	Leu	Ser	Met	Lys	Ala	Ala	Phe	Gly	Lys
225						230					235				240
gtt	tgg	aag	ctg	gaa	aaa	aat	ggg	gtt	agc	att	att	ggg	act	tcc	
Val	Trp	Lys	Leu	Glu	Lys	Asn	Gly	Gly	Ser	Ile	Ile	Gly	Gly	Thr	Phe
						245					250				255
aaa	gca	ata	caa	gag	aga	aat	gga	gct	tca	aaa	cca	cct	cga	gat	ccg
Lys	Ala	Ile	Gln	Glu	Arg	Asn	Gly	Ala	Ser	Lys	Pro	Pro	Arg	Asp	Pro
						260					265				270
cgt	ctg	cca	aaa	cca	aaa	ggg	cag	act	gtt	gga	tct	tcc	cgg	aag	ggg
Arg	Leu	Pro	Lys	Pro	Lys	Gly	Gln	Thr	Val	Gly	Ser	Phe	Arg	Lys	Gly
						275					280				285
ctt	acc	atg	ttg	cct	gat	gca	att	tct	gcc	aga	cta	ggc	aac	aaa	gta
Leu	Thr	Met	Leu	Pro	Asp	Ala	Ile	Ser	Ala	Arg	Leu	Gly	Asn	Lys	Val
						290					295				300
aag	tta	tct	tgg	aag	ctt	tca	agt	att	agt	aaa	ctg	gat	agt	gga	gag
Lys	Leu	Ser	Trp	Lys	Leu	Ser	Ser	Ile	Ser	Lys	Leu	Asp	Ser	Gly	Glu
						305					310				320
tac	agt	ttg	aca	tat	gaa	aca	cca	gaa	gga	gtg	gtt	tct	ttg	cag	tgc
Tyr	Ser	Leu	Thr	Tyr	Glu	Thr	Pro	Glu	Gly	Val	Val	Ser	Leu	Gln	Cys
						325					330				335
aaa	act	gtt	gtc	ctg	acc	att	cct	tcc	tat	gtt	gct	agt	aca	ttg	ctg
Lys	Thr	Val	Val	Leu	Thr	Ile	Pro	Ser	Tyr	Val	Ala	Ser	Thr	Leu	Leu
						340					345				350
cgt	cct	ctg	tct	gtc	gtc	gca	gat	gca	ctt	tca	aag	ttt	tat	tac	
Arg	Pro	Leu	Ser	Ala	Ala	Ala	Asp	Ala	Leu	Ser	Lys	Phe	Tyr	Tyr	
						355					360				365
cct	cca	gtt	gct	gca	gtt	tcc	ata	tcc	tat	cca	aaa	gaa	gct	att	aga
Pro	Pro	Val	Ala	Ala	Val	Ser	Ile	Ser	Tyr	Pro	Lys	Glu	Ala	Ile	Arg
						370					375				380
tca	gaa	tgc	ttg	ata	gat	ggg	gag	ttg	aag	ggg	ttt	gtt	caa	ttg	cat
Ser	Glu	Cys	Leu	Ile	Asp	Gly	Glu	Leu	Lys	Gly	Phe	Gly	Gln	Leu	His
						385					390				400
cca	cgt	agg	caa	gga	gtg	gaa	aca	tta	gga	act	ata	tac	agc	tca	tca
Pro	Arg	Ser	Gln	Gly	Val	Glu	Thr	Leu	Gly	Thr	Ile	Tyr	Ser	Ser	Ser
						405					410				415
cta	ttc	ccc	aac	cga	gca	cca	cct	gga	agg	gtt	cta	ctc	ttg	aat	tac
Leu	Phe	Pro	Asn	Arg	Ala	Pro	Pro	Gly	Arg	Val	Leu	Leu	Asn	Tyr	
						420					425				430
att	gga	gga	gca	act	aat	act	gga	att	tta	tcg	aag	acg	gac	agt	gaa
Ile	Gly	Gly	Ala	Thr	Asn	Thr	Gly	Ile	Leu	Ser	Lys	Thr	Asp	Ser	Glu
						435					440				445
ctt	gtg	gaa	aca	gtt	gat	cga	gat	ttg	agg	aaa	atc	ctt	ata	aac	cca
Leu	Val	Glu	Thr	Val	Asp	Arg	Asp	Leu	Arg	Lys	Ile	Leu	Ile	Asn	Pro
						450					455				460
aat	gcc	cag	gat	cca	ttt	gtt	gtg	ggg	gtg	aga	ctg	tgg	caa	gct	
Asn	Ala	Gln	Asp	Pro	Phe	Val	Val	Gly	Val	Arg	Leu	Trp	Pro	Gln	Ala
						465					470				480
att	cca	cag	ttc	tta	gtt	ggc	cat	ctt	gat	ctt	cta	gat	gtt	gct	aaa

Ile Pro Gln Phe Leu Val Gly His Leu Asp Leu Leu Asp Val Ala Lys				
485	490	495		
gct tct atc aga aat act ggg ttt gaa ggg ctc ttc ctt ggg ggt aat				1536
Ala Ser Ile Arg Asn Thr Gly Phe Glu Gly Leu Phe Leu Gly Gly Asn				
500	505	510		
tat gtg tct ggt gtt gcc ttg gga cga tgc gtt gag gga gcc tat gag				1584
Tyr Val Ser Gly Val Ala Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu				
515	520	525		
gta gca gct gaa gta aac gat ttt ctc aca aat aga gtg tac aaa tag				1632
Val Ala Ala Glu Val Asn Asp Phe Leu Thr Asn Arg Val Tyr Lys				
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<212> PRT
<213> Glycine max var. Williams82

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20	25	30		
Arg Lys Phe Pro Arg Ser Arg Pro Asn Pro Ile Leu Arg Cys Ser Ile				
35	40	45		
Ala Glu Glu Ser Thr Ala Ser Pro Pro Lys Thr Arg Asp Ser Ala Pro				
50	55	60		
Val Asp Cys Val Val Gly Gly Val Ser Gly Leu Cys Ile Ala				
65	70	75	80	
Gln Ala Leu Ala Thr Lys His Ala Asn Ala Asn Val Val Val Thr Glu				
85	90	95		
Ala Arg Asp Arg Val Gly Gly Asn Ile Thr Thr Met Glu Arg Asp Gly				
100	105	110		
Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met				
115	120	125		
Leu Thr Met Val Val Asp Ser Gly Leu Lys Asp Glu Leu Val Leu Gly				
130	135	140		
Asp Pro Asp Ala Pro Arg Phe Val Leu Trp Asn Arg Lys Leu Arg Pro				
145	150	155	160	
Val Pro Gly Lys Leu Thr Asp Leu Pro Phe Phe Asp Leu Met Ser Ile				
165	170	175		
Gly Gly Lys Ile Arg Ala Gly Phe Gly Ala Leu Gly Ile Arg Pro Pro				
180	185	190		
Pro Pro Gly His Glu Glu Ser Val Glu Glu Phe Val Arg Arg Asn Leu				
195	200	205		
Gly Asp Glu Val Phe Glu Arg Leu Ile Glu Pro Phe Cys Ser Gly Val				
210	215	220		
Tyr Ala Gly Asp Pro Ser Lys Leu Ser Met Lys Ala Ala Phe Gly Lys				
225	230	235	240	
Val Trp Lys Leu Glu Lys Asn Gly Gly Ser Ile Ile Gly Gly Thr Phe				
245	250	255		
Lys Ala Ile Gln Glu Arg Asn Gly Ala Ser Lys Pro Pro Arg Asp Pro				
260	265	270		
Arg Leu Pro Lys Pro Lys Gly Gln Thr Val Gly Ser Phe Arg Lys Gly				
275	280	285		
Leu Thr Met Leu Pro Asp Ala Ile Ser Ala Arg Leu Gly Asn Lys Val				
290	295	300		
Lys Leu Ser Trp Lys Leu Ser Ser Ile Ser Lys Leu Asp Ser Gly Glu				

305	310	315	320
Tyr Ser Leu Thr Tyr Glu Thr Pro Glu Gly Val Val Ser Leu Gln Cys			
325	330	335	
Lys Thr Val Val Leu Thr Ile Pro Ser Tyr Val Ala Ser Thr Leu Leu			
340	345	350	
Arg Pro Leu Ser Ala Ala Ala Asp Ala Leu Ser Lys Phe Tyr Tyr			
355	360	365	
Pro Pro Val Ala Ala Val Ser Ile Ser Tyr Pro Lys Glu Ala Ile Arg			
370	375	380	
Ser Glu Cys Leu Ile Asp Gly Glu Leu Lys Gly Phe Gly Gln Leu His			
385	390	395	400
Pro Arg Ser Gln Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser			
405	410	415	
Leu Phe Pro Asn Arg Ala Pro Pro Gly Arg Val Leu Leu Leu Asn Tyr			
420	425	430	
Ile Gly Gly Ala Thr Asn Thr Gly Ile Leu Ser Lys Thr Asp Ser Glu			
435	440	445	
Leu Val Glu Thr Val Asp Arg Asp Leu Arg Lys Ile Leu Ile Asn Pro			
450	455	460	
Asn Ala Gln Asp Pro Phe Val Val Gly Val Arg Leu Trp Pro Gln Ala			
465	470	475	480
Ile Pro Gln Phe Leu Val Gly His Leu Asp Leu Leu Asp Val Ala Lys			
485	490	495	
Ala Ser Ile Arg Asn Thr Gly Phe Glu Gly Leu Phe Leu Gly Gly Asn			
500	505	510	
Tyr Val Ser Gly Val Ala Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu			
515	520	525	
Val Ala Ala Glu Val Asn Asp Phe Leu Thr Asn Arg Val Tyr Lys			
530	535	540	543

<210> 7
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify bchH gene

<400> 7
gacatctagt ctagacgacc atatgcacgg tgaagtctc 39

<210> 8
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
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<400> 8
acggaagctt ggtacacctac tcggcgccaa t 31

<210> 9
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify DNA fragment having partial sequence of tobacco chlH gene

<400> 9
ccaatgtata gctatggta cttatgttatt cactc 35

<210> 10
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify DNA fragment having partial sequence of tobacco chlH gene

<400> 10
gagatcattc ttttgctgt cgacttatcg atcg 34

<210> 11
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify DNA fragment having partial sequence of soybean PPO gene

<400> 11
ggcgaggcg tcaccatggt ctgcatcgcc caggcc 36

<210> 12
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify DNA fragment having partial sequence of soybean PPO gene

<400> 12
gcctgcaggc cgacaactgc tactatgtt acactc 36

<210> 13
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify DNA fragment having partial sequence of soybean PPO gene

<400> 13
cacaggaaag gtaccatggt ctgcatcgcc cag 33

<210> 14
<211> 33

<212> DNA
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<220>
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<400> 14
 cctgcagtc gagagctcct actatttgt a c a c 33

<210> 15
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to amplify Chlamydomonas PPO gene

<400> 15
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<210> 16
 <211> 27
 <212> DNA
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 <223> Designed oligonucleotide primer to amplify Chlamydomonas PPO gene

<400> 16
 tactacacat cccagcaagc gccaatg 27

<210> 17
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 <212> DNA
 <213> Chlamydomonas reinhardtii CC407

<220>
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 <222> (1)...(1693)

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 Arg Ser Gln Ile Arg Ser Ala Ala His Val Ser Ala Lys Val Ala Pro
 20 25 30
 c g g c c a c g c c a t t c t c g g c g a g c c c g c g a c c g c t g g g a g c c c 142
 Arg Pro Thr Pro Phe Ser Val Ala Ser Pro Ala Thr Ala Ala Ser Pro
 35 40 45
 g c g a c c g c g g c c c g c a c t c t c a c g c g a c t g c t g c g g c g g c c 190
 Ala Thr Ala Ala Ala Arg Arg Thr Leu His Arg Thr Ala Ala Ala Ala
 50 55 60
 a c t g g t g c t c c a c g g c g t c c g g a g c g c t c g a c g t c g a c 238
 Thr Gly Ala Pro Thr Ala Ser Gly Ala Gly Val Ala Lys Thr Leu Asp
 65 70 75

aat gtg tat gac gtc atc gtc gtc ggt gga ggt ctc tcg ggc ctg gtg	286
Asn Val Tyr Asp Val Ile Val Val Gly Gly Leu Ser Gly Leu Val	
80 85 90 95	
acc ggc cag gcc ctg gcg gct cag cac aaa att cag aac ttc ctt gtt	334
Thr Gly Gln Ala Leu Ala Ala Gln His Lys Ile Gln Asn Phe Leu Val	
100 105 110	
acg gag gct cgc gag cgc gtc ggc ggc aac att acg tcc atg tcg ggc	382
Thr Glu Ala Arg Glu Arg Val Gly Gly Asn Ile Thr Ser Met Ser Gly	
115 120 125	
gat ggc tac gtg tgg gag gag ggc ccg aac agc ttc cag ccc aac gat	430
Asp Gly Tyr Val Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Asn Asp	
130 135 140	
agc atg ctg cag att gcg gtg gac tct ggc tgc gag aag gac ctt gtg	478
Ser Met Leu Gln Ile Ala Val Asp Ser Gly Cys Glu Lys Asp Leu Val	
145 150 155	
ttc ggt gac ccc acg gct ccc cgc ttc gtg tgg tgg gag ggc aag ctg	526
Phe Gly Asp Pro Thr Ala Pro Arg Phe Val Trp Trp Glu Gly Lys Leu	
160 165 170 175	
cgc ccc gtg ccc tcg ggc ctg gac gcc ttc acc ttc gac ctc atg tcc	574
Arg Pro Val Pro Ser Gly Leu Asp Ala Phe Thr Phe Asp Leu Met Ser	
180 185 190	
atc ccc ggc aag atc cgc gcc ggg ctg ggc gcc atc ggc ctc atc aac	622
Ile Pro Gly Ile Arg Ala Gly Leu Gly Ala Ile Gly Leu Ile Asn	
195 200 205	
gga gcc atg ccc tcc ttc gag gag agt gtg gag cag ttc atc cgc cgc	670
Gly Ala Met Pro Ser Phe Glu Ser Val Glu Gln Phe Ile Arg Arg	
210 215 220	
aac ctg ggc gat gag gtg ttc ctc cgc ctg atc gag ccc ttc tgc tcc	718
Asn Leu Gly Asp Glu Val Phe Arg Leu Ile Glu Pro Phe Cys Ser	
225 230 235	
ggc gtg tac gcg ggc gac ccc tcc aag ctg tcc atg aag gcg gcc ttc	766
Gly Val Tyr Ala Gly Asp Pro Ser Lys Leu Ser Met Lys Ala Ala Phe	
240 245 250 255	
aac agg atc tgg att ctg gag aag aac ggc ggc agc ctg gtg gga ggt	814
Asn Arg Ile Trp Ile Leu Glu Lys Asn Gly Gly Ser Leu Val Gly Gly	
260 265 270	
gcc atc aag ctg ttc cag gaa cgc cag tcc aac ccg gcc ccc cgg	862
Ala Ile Lys Leu Phe Gln Glu Arg Gln Ser Asn Pro Ala Pro Pro Arg	
275 280 285	
gac ccg cgc ctg ccg ccc aag ccc aag ggc cag acg gtg ggc tcg ttc	910
Asp Pro Arg Leu Pro Pro Lys Pro Lys Gly Gln Thr Val Gly Ser Phe	
290 295 300	
cgc aag ggc ctg aag atg ctg ccg gac gcc att gag cgc aac atc ccc	958
Arg Lys Gly Leu Lys Met Leu Pro Asp Ala Ile Glu Arg Asn Ile Pro	
305 310 315	
gac aag atc cgc gtg aac tgg aag ctg gtg tct ctg ggc cgc gag gcg	1006
Asp Lys Ile Arg Val Asn Trp Lys Leu Val Ser Leu Gly Arg Glu Ala	
320 325 330 335	
gac ggg cgg tac ggg ctg gtg tac gac acg ccc gag ggc cgt gtc aag	1054
Asp Gly Arg Tyr Gly Leu Val Tyr Asp Thr Pro Glu Gly Arg Val Lys	
340 345 350	
gtg ttt gcc cgc gcc gtg gct ctg acc gcg ccc agc tac gtg gtg gcg	1102
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355 360 365	
gac ctg gtc aag gag cag gcg ccc gcc gcc gag ggc ctg ggc tcc	1150
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370 375 380	

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ggt cag ctg cac ccg cgc acc cag ggc atc acc act ctg ggc acc atc Gly Gln Leu His Pro Arg Thr Gln Gly Ile Thr Thr Leu Gly Thr Ile	1294
420 425 430	
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435 440 445	
ctg ctc aac tac atc ggc ggc acc acc aac cgc ggc atc gtc aac cag Leu Leu Asn Tyr Ile Gly Gly Thr Thr Asn Arg Gly Ile Val Asn Gln	1390
450 455 460	
acc acc gag cag ctg gtg gag cag gtg gac aag gac ctg cgc aac atg Thr Thr Glu Gln Leu Val Glu Gln Val Asp Lys Asp Leu Arg Asn Met	1438
465 470 475	
gtc atc aag ccc gac gcg ccc aag ccc cgt gtg gtg ggc gtg cgc gtg Val Ile Lys Pro Asp Ala Pro Lys Pro Arg Val Val Gly Val Arg Val	1486
480 485 490 495	
tgg ccg cgc gcc atc ccg cag ttc aac ctg ggc cac ctg gag cag ctg Trp Pro Arg Ala Ile Pro Gln Phe Asn Leu Gly His Leu Glu Gln Leu	1534
500 505 510	
gac aag gcg cgc aag gcg ctg gac gcg gcg ggg ctg cag ggc gtg cac Asp Lys Ala Arg Lys Ala Leu Asp Ala Ala Gly Leu Gln Gly Val His	1582
515 520 525	
ctg ggg ggc aac tac gtc agc ggt gtg gcc ctg ggc aag gtg gtg gag Leu Gly Gly Asn Tyr Val Ser Gly Val Ala Leu Gly Lys Val Val Glu	1630
530 535 540	
cac ggc tac gag tcc gca gcc aac ctg gcc aag agc gtg tcc aag gcc His Gly Tyr Glu Ser Ala Ala Asn Leu Ala Lys Ser Val Ser Lys Ala	1678
545 550 555	
gca gtc aag gcc taa gcggctgcag cagtagcagc agcagcatcg ggctgttagct Ala Val Lys Ala	1733
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Arg Pro Thr Pro Phe Ser Val Ala Ser Pro Ala Thr Ala Ala Ser Pro 35 40 45	
Ala Thr Ala Ala Ala Arg Arg Thr Leu His Arg Thr Ala Ala Ala Ala 50 55 60	
Thr Gly Ala Pro Thr Ala Ser Gly Ala Gly Val Ala Lys Thr Leu Asp 65 70 75	
Asn Val Tyr Asp Val Ile Val Val Gly Gly Leu Ser Gly Leu Val	

80	85	90	95
Thr Gly Gln Ala Leu Ala Ala Gln His Lys Ile Gln Asn Phe Leu Val			
100	105	110	
Thr Glu Ala Arg Glu Arg Val Gly Gly Asn Ile Thr Ser Met Ser Gly			
115	120	125	
Asp Gly Tyr Val Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Asn Asp			
130	135	140	
Ser Met Leu Gln Ile Ala Val Asp Ser Gly Cys Glu Lys Asp Leu Val			
145	150	155	
Phe Gly Asp Pro Thr Ala Pro Arg Phe Val Trp Trp Glu Gly Lys Leu			
160	165	170	175
Arg Pro Val Pro Ser Gly Leu Asp Ala Phe Thr Phe Asp Leu Met Ser			
180	185	190	
Ile Pro Gly Lys Ile Arg Ala Gly Leu Gly Ala Ile Gly Leu Ile Asn			
195	200	205	
Gly Ala Met Pro Ser Phe Glu Glu Ser Val Glu Gln Phe Ile Arg Arg			
210	215	220	
Asn Leu Gly Asp Glu Val Phe Phe Arg Leu Ile Glu Pro Phe Cys Ser			
225	230	235	
Gly Val Tyr Ala Gly Asp Pro Ser Lys Leu Ser Met Lys Ala Ala Phe			
240	245	250	255
Asn Arg Ile Trp Ile Leu Glu Lys Asn Gly Gly Ser Leu Val Gly Gly			
260	265	270	
Ala Ile Lys Leu Phe Gln Glu Arg Gln Ser Asn Pro Ala Pro Pro Arg			
275	280	285	
Asp Pro Arg Leu Pro Pro Lys Pro Lys Gly Gln Thr Val Gly Ser Phe			
290	295	300	
Arg Lys Gly Leu Lys Met Leu Pro Asp Ala Ile Glu Arg Asn Ile Pro			
305	310	315	
Asp Lys Ile Arg Val Asn Trp Lys Leu Val Ser Leu Gly Arg Glu Ala			
320	325	330	335
Asp Gly Arg Tyr Gly Leu Val Tyr Asp Thr Pro Glu Gly Arg Val Lys			
340	345	350	
Val Phe Ala Arg Ala Val Ala Leu Thr Ala Pro Ser Tyr Val Val Ala			
355	360	365	
Asp Leu Val Lys Glu Gln Ala Pro Ala Ala Glu Ala Leu Gly Ser			
370	375	380	
Phe Asp Tyr Pro Pro Val Gly Ala Val Thr Leu Ser Tyr Pro Leu Ser			
385	390	395	
Ala Val Arg Glu Glu Arg Lys Ala Ser Asp Gly Ser Val Pro Gly Phe			
400	405	410	415
Gly Gln Leu His Pro Arg Thr Gln Gly Ile Thr Thr Leu Gly Thr Ile			
420	425	430	
Tyr Ser Ser Ser Leu Phe Pro Gly Arg Ala Pro Glu Gly His Met Leu			
435	440	445	
Leu Leu Asn Tyr Ile Gly Gly Thr Thr Asn Arg Gly Ile Val Asn Gln			
450	455	460	
Thr Thr Glu Gln Leu Val Glu Gln Val Asp Lys Asp Leu Arg Asn Met			
465	470	475	
Val Ile Lys Pro Asp Ala Pro Lys Pro Arg Val Val Gly Val Arg Val			
480	485	490	495
Trp Pro Arg Ala Ile Pro Gln Phe Asn Leu Gly His Leu Glu Gln Leu			
500	505	510	
Asp Lys Ala Arg Lys Ala Leu Asp Ala Ala Gly Leu Gln Gly Val His			
515	520	525	
Leu Gly Gly Asn Tyr Val Ser Gly Val Ala Leu Gly Lys Val Val Glu			
530	535	540	

His Gly Tyr Glu Ser Ala Ala Asn Leu Ala Lys Ser Val Ser Lys Ala
545 550 555
Ala Val Lys Ala
560 563

<210> 19
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify DNA fragment having partial sequence of Chlamydomonas PPO gene

<400> 19
ggtcgggtgga ggggatccga tgctggtgac cg 32

<210> 20
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify DNA fragment having partial sequence of Chlamydomonas PPO gene

<400> 20
gctactgctg cgagctctta ggccttgact gc 32

<210> 21
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify DNA fragment having partial sequence of cucumber ferrochelatase gene

<400> 21
gctttagaat cggatcctat ggcagtggat gac 33

<210> 22
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify DNA fragment having partial sequence of cucumber ferrochelatase gene

<400> 22
ggtaacctc tattttagct ctcaggtaaa tataag 36

<210> 23
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify Esherichia coli hemF gene

<400> 23
gctgaaggcg tgatcagtta tttcc 25

<210> 24
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify Esherichia coli hemF gene

<400> 24
catcagcctg cagtgcgaaa agtg 24

<210> 25
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify Esherichia coli hemF gene

<400> 25
cgaaaaaggg atccgttatg aaaccc 26

<210> 26
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify Esherichia coli hemF gene

<400> 26
gctgtttcc gagctcccgt cac 23

<210> 27
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotides to synthesize genes encoding random peptides comprising 5 amino acids

<220>
<221> unsure
<222> (1)...(22)
<223> any n = a, g, c, t, any, unknown, or other

<400> 27
tggccnnknn knnknnknn gc 22

<210> 28
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotides to synthesize genes encoding random peptides comprising 5 amino acids

<220>
<221> unknown
<222> (1)...(29)
<223> any n = a, g, c, t, any, unknown, or other

<400> 28
ggccgcnnnn nnnnnnnnnnn nggccagct 29

<210> 29
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to synthesize the gene encoding the peptide HASYS

<400> 29
tggcccatgc tagtttagtcg gc 22

<210> 30
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to synthesize the gene encoding the peptide HASYS

<400> 30
tggcgccgac taactagcat gggccagct 29

<210> 31
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to synthesize the gene encoding the peptide RASSL

<400> 31
tggcccgggc gtcgtcgttg gc 22

<210> 32
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to synthesize the gene encoding the peptide RASSL

<400> 32
ggccgccaac gacgacgccc gggccagct 29

<210> 33
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to synthesize the gene encoding the peptide
MGHASYS

<400> 33
catgggtcac gcttcttact cctaag 26

<210> 34
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to synthesize the gene encoding the peptide
MGHASYS

<400> 34
aattcttagg agtaagaagc gtgacc 26

<210> 35
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to synthesize the gene encoding the peptide
MGRASSL

<400> 35
catgggtcgt gcttcttccc tgtaag 26

<210> 36
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to synthesize the gene encoding the peptide
MGRASSL

<400> 36
aattcttaca ggaaagaagc acgacc 26

<210> 37
<211> 23
<212> DNA
<213> Artificial Sequence

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<220>
<223> Designed oligonucleotide to synthesize the gene encoding the peptide
MGYAGY

<400> 37
catgggttac gctggctact aag  23

<210> 38
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to synthesize the gene encoding the peptide
MGYAGY

<400> 38
aattcttagt agccagcgta acc  23

<210> 39
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to synthesize the gene encoding the peptide
MGYAGF

<400> 39
catgggttac gctggcttct aag  23

<210> 40
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to synthesize the gene encoding the peptide
MGYAGF

<400> 40
aattcttaga agccagcgta acc  23

<210> 41
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to synthesize the gene encoding the peptide
MG(HASYS)4

<400> 41
catgggtcac gcttcttact cccatgcac ttac  34

<210> 42
<211> 36
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<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to synthesize the gene encoding the peptide
MG(HASYS) 4

<400> 42
gtgggagtaa gatgcattgg agtaagaagc gtgacc 36

<210> 43
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to synthesize the gene encoding the peptide
MG(HASYS) 4

<400> 43
tcccacgctt cttactccca tgcattttac tcctaag 37

<210> 44
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to synthesize the gene encoding the peptide
MG(HASYS) 4

<400> 44
aattcttagg agtaagatgc atgggagtaa gaagc 35

<210> 45
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to synthesize the gene encoding the peptide
MG(HASYS) 8

<400> 45
tcccacgctt cttactccca tgcattttac 30

<210> 46
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to synthesize the gene encoding the peptide
MG(HASYS) 8

<400> 46
gtgggagtaa gatgcattgg agtaagaagc 30

<210> 47
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to synthesize the gene encoding the peptide
MG(RASSL) 4

<400> 47
catgggtcgt gcttcttccc tgcgcgcata ttcc 34

<210> 48
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to synthesize the gene encoding the peptide
MG(RASSL) 4

<400> 48
acgcaggaa gatgcgcga gggagaagaacg acgacc 36

<210> 49
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to synthesize the gene encoding the peptide
MG(RASSL) 4

<400> 49
ctgcgtgtt cttccctgcg cgcatcttcc ctgttaag 37

<210> 50
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to synthesize the gene encoding the peptide
MG(RASSL) 4

<400> 50
aattcttaca ggaaagatgc ggcaggaa gaagc 35

<210> 51
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to synthesize the gene encoding the peptide
MG(RASSL) 8

<400> 51
ctgcgtgctt cttccctgcg cgcatcttcc 30

<210> 52
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to synthesize the gene encoding the peptide MG(RASSL)8

<400> 52
acgcaggaa gatgcgcga ggaaagaagc 30

<210> 53
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Protoporphyrin IX binding protein HASYS

<400> 53
His Ala Ser Tyr Ser
1 5

<210> 54
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Protoporphyrin IX binding protein MGHASYS

<400> 54
Met Gly His Ala Ser Tyr Ser
1 5

<210> 55
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Protoporphyrin IX binding protein RASSL

<400> 55
Arg Ala Ser Ser Leu
1 5

<210> 56
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Protoporphyrin IX binding protein MGRASSL

<400> 56
Met Gly Arg Ala Ser Ser Leu
1 5

<210> 57
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> H2TMPyP binding protein YAGY.

<400> 57
Tyr Ala Gly Tyr

<210> 58
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> H2TMPyP binding protein MGYAGY

<400> 58
Met Gly Tyr Ala Gly Tyr
1 5

<210> 59
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> H2TMPyP binding protein YAGF

<400> 59
Tyr Ala Gly Phe
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<210> 60
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> H2TMPyP binding protein MGYAGF

<400> 60
Met Gly Tyr Ala Gly Phe
1 5

<210> 61
<211> 22
<212> PRT

<213> Artificial Sequence

<220>

<223> Protoporphyrin IX binding protein MG(HASYS)4

<400> 61

Met Gly His Ala Ser Tyr Ser His Ala Ser Tyr Ser His Ala Ser Tyr
1 5 10 15
Ser His Ala Ser Tyr Ser
20

<210> 62

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> Protoporphyrin IX binding protein MG(HASYS)8

<400> 62

Met Gly His Ala Ser Tyr Ser His Ala Ser Tyr Ser His Ala Ser Tyr
1 5 10 15
Ser His Ala Ser Tyr Ser His Ala Ser Tyr Ser His Ala Ser Tyr Ser
20 25 30
His Ala Ser Tyr Ser His Ala Ser Tyr Ser
35 40

<210> 63

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Protoporphyrin IX binding protein MG(RASSL)4

<400> 63

Met Gly Arg Ala Ser Ser Leu Arg Ala Ser Ser Leu Arg Ala Ser Ser
1 5 10 15
Leu Arg Ala Ser Ser Leu
20

<210> 64

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> Protoporphyrin IX binding protein MG(RASSL)8.

<400> 64

Met Gly Arg Ala Ser Ser Leu Arg Ala Ser Ser Leu Arg Ala Ser Ser
1 5 10 15
Leu Arg Ala Ser Ser Leu Arg Ala Ser Ser Leu Arg Ala Ser Ser Leu
20 25 30
Arg Ala Ser Ser Leu Arg Ala Ser Ser Leu
35 40

<210> 65
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to introduce mutation into arabidopsis PPO gene

<400> 65
tgttcaggtg tttatgttgg tgatccttca aaactg 36

<210> 66
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify herbicide resistant arabidopsis PPO(A220V) gene

<400> 66
ccatgcgaa gcttatggag ttatctcttc tc 32

<210> 67
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify herbicide resistant arabidopsis PPO(A220V) gene

<400> 67
gggagattta atgtcgacca tttacttgta agcg 34

<210> 68
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify Arabidopsis chloroplast ferrochelatase gene

<400> 68
gatcggttct gaaatttggaa tccatgcagg c 31

<210> 69
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify Arabidopsis chloroplast ferrochelatase gene

<400> 69
cacaaaacca acgagtcct ataggttccg g 31

<210> 70
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify soybean coproporphyrinogen III oxidase gene

<400> 70
gaatcggtc cgaaggcatga tgcatttgtgc 30

<210> 71
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify soybean coproporphyrinogen III oxidase gene

<400> 71
gggggtcgac tgcatgttta gatccattcc 30

<210> 72
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify DNA fragment having nucleotide sequence encoding the Petunia hybrida EPSPS chloroplast transit peptide and the Agrobacterium sp. strain CP4 EPSPS gene

<400> 72
gaaagcttca agaatggcac aaatttacaa catggc 36

<210> 73
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify DNA fragment having nucleotide sequence encoding the Petunia hybrida EPSPS chloroplast transit peptide and the Agrobacterium sp. strain CP4 EPSPS gene

<400> 73
gagtcgacgg tcatcaggca gccttcgtat cg 32

<210> 74
<211> 1587
<212> DNA

<213> Petunia hybrida EPSPS chloroplast transit peptide and Agrobacterium sp.
strain CP4 EPSPS

<220>

<221> CDS

<222> (1)...(1581)

<400> 74

atg gca caa att aac aac atg gct caa ggg ata caa acc ctt aat ccc Met Ala Gln Ile Asn Asn Met Ala Gln Gly Ile Gln Thr Leu Asn Pro	48
1 5 10 15	
aat tcc aat ttc cat aaa ccc caa gtt cct aaa tct tca agt ttt ctt Asn Ser Asn Phe His Lys Pro Gln Val Pro Lys Ser Ser Phe Leu	96
20 25 30	
gtt ttt gga tct aaa aaa ctg aaa aat tca gca aat tct atg ttg gtt Val Phe Gly Ser Lys Lys Leu Lys Asn Ser Ala Asn Ser Met Leu Val	144
35 40 45	
ttg aaa aaa gat tca att ttt atg caa aag ttt tgt tcc ttt agg att Leu Lys Lys Asp Ser Ile Phe Met Gln Lys Phe Cys Ser Phe Arg Ile	192
50 55 60	
tca gca tca gtg gct aca gcc tgc atg ctt cac ggt gca agc agc cgg Ser Ala Ser Val Ala Thr Ala Cys Met Leu His Gly Ala Ser Ser Arg	240
65 70 75 80	
ccc gca acc gcc cgc aaa tcc tct ggc ctt tcc gga acc gtc cgc att Pro Ala Thr Ala Arg Lys Ser Ser Gly Leu Ser Gly Thr Val Arg Ile	288
85 90 95	
ccc ggc gac aag tcg atc tcc cac cgg tcc ttc atg ttc ggc ggt ctc Pro Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly Leu	336
100 105 110	
gcg agc ggt gaa acg cgc att acc ggc ctt ctg gaa ggc gag gac gtc Ala Ser Gly Glu Thr Arg Ile Thr Gly Leu Leu Glu Gly Glu Asp Val	384
115 120 125	
atc aat acg ggc aag gcc atg cag gcc atg ggc gcc agg atc cgt aag Ile Asn Thr Gly Lys Ala Met Gln Ala Met Gly Ala Arg Ile Arg Lys	432
130 135 140	
gaa ggc gac acc tgg atc atc gat ggc gtc ggc aat ggc ggc ctc ctg Glu Gly Asp Thr Trp Ile Ile Asp Gly Val Gly Asn Gly Gly Leu Leu	480
145 150 155 160	
gcg cct gag ggc ccc ctc gat ttc ggc aat gcc gcc acg ggc tgc cgc Ala Pro Glu Ala Pro Leu Asp Phe Gly Asn Ala Ala Thr Gly Cys Arg	528
165 170 175	
ctg acc atg ggc ctc gtc ggg gtc tac gat ttc gac agc acc ttc atc Leu Thr Met Gly Leu Val Gly Val Tyr Asp Phe Asp Ser Thr Phe Ile	576
180 185 190	
ggc gac gcc tcg ctc aca aag cgc ccg atg ggc cgc gtg ttg aac ccg Gly Asp Ala Ser Leu Thr Lys Arg Pro Met Gly Arg Val Leu Asn Pro	624
195 200 205	
ctg cgc gaa atg ggc gtg cag gtg aaa tcg gaa gac ggt gac cgt ctt Leu Arg Glu Met Gly Val Gln Val Lys Ser Glu Asp Gly Asp Arg Leu	672
210 215 220	
ccc gtt acc ttg cgc ggg ccg aag acg ccg acg ccg atc acc tac cgc Pro Val Thr Leu Arg Gly Pro Lys Thr Pro Thr Pro Ile Thr Tyr Arg	720
225 230 235 240	
gtg ccg atg gcc tcc gca cag gtg aag tcc gcc gtg ctg ctc gcc ggc Val Pro Met Ala Ser Ala Gln Val Lys Ser Ala Val Leu Leu Ala Gly	768
245 250 255	
ctc aac acg ccc ggc atc acg acg gtc atc gag ccg atc atg acg cgc	816

Leu Asn Thr Pro Gly Ile Thr Thr Val Ile Glu Pro Ile Met Thr Arg			
260	265	270	
gat cat acg gaa aag atg ctg cag ggc ttt ggc gcc aac ctt acc gtc			864
Asp His Thr Glu Lys Met Leu Gln Gly Phe Gly Ala Asn Leu Thr Val			
275	280	285	
gag acg gat gcg gac ggc gtg cgc acc atc cgc ctg gaa ggc cgc ggc			912
Glu Thr Asp Ala Asp Gly Val Arg Thr Ile Arg Leu Glu Gly Arg Gly			
290	295	300	
aag ctc acc ggc caa gtc atc gac gtg ccg ggc gac ccg tcc tcg acg			960
Lys Leu Thr Gly Gln Val Ile Asp Val Pro Gly Asp Pro Ser Ser Thr			
305	310	315	320
gcc ttc ccg ctg gtt gcg gcc ctg ctt gtt ccg ggc tcc gac gtc acc			1008
Ala Phe Pro Leu Val Ala Ala Leu Leu Val Pro Gly Ser Asp Val Thr			
325	330	335	
atc ctc aac gtg ctg atg aac ccc acc cgc acc ggc ctc atc ctg acg			1056
Ile Leu Asn Val Leu Met Asn Pro Thr Arg Thr Gly Leu Ile Leu Thr			
340	345	350	
ctg cag gaa atg ggc gac atc gaa gtc atc aac ccg cgc ctt gcc			1104
Leu Gln Glu Met Gly Ala Asp Ile Glu Val Ile Asn Pro Arg Leu Ala			
355	360	365	
ggc ggc gaa gac gtg gcg gac ctg cgc gtt cgc tcc tcc acg ctg aag			1152
Gly Gly Glu Asp Val Ala Asp Leu Arg Val Arg Ser Ser Thr Leu Lys			
370	375	380	
ggc gtc acg gtg ccg gaa gac cgc gcg cct tcg atg atc gac gaa tat			1200
Gly Val Thr Val Pro Glu Asp Arg Ala Pro Ser Met Ile Asp Glu Tyr			
385	390	395	400
ccg att ctc gct gtc gcc gcc ttc gcg gaa ggg ggc acc gtg atg			1248
Pro Ile Leu Ala Val Ala Ala Ala Phe Ala Glu Gly Ala Thr Val Met			
405	410	415	
aac ggt ctg gaa gaa ctc cgc gtc aag gaa agc gac cgc ctc tcg gcc			1296
Asn Gly Leu Glu Leu Arg Val Lys Glu Ser Asp Arg Leu Ser Ala			
420	425	430	
gtc gcc aat ggc ctc aag ctc aat ggc gtg gat tgc gat gag ggc gag			1344
Val Ala Asn Gly Leu Lys Leu Asn Gly Val Asp Cys Asp Glu Gly Glu			
435	440	445	
acg tcg ctc gtc gtc cgc ggc cct gac ggc aag ggg ctc ggc aac			1392
Thr Ser Leu Val Val Arg Gly Arg Pro Asp Gly Lys Gly Leu Gly Asn			
450	455	460	
gcc tcg ggc gcc gtc gcc acc cat ctc gat cac cgc atc gcc atg			1440
Ala Ser Gly Ala Ala Val Ala Thr His Leu Asp His Arg Ile Ala Met			
465	470	475	480
agc ttc ctc gtc atg ggc ctc gtg tcg gaa aac cct gtc acg gtg gac			1488
Ser Phe Leu Val Met Gly Leu Val Ser Glu Asn Pro Val Thr Val Asp			
485	490	495	
gat gcc acg atg atc gcc acg agc ttc ccg gag ttc atg gac ctg atg			1536
Asp Ala Thr Met Ile Ala Thr Ser Phe Pro Glu Phe Met Asp Leu Met			
500	505	510	
gcc ggg ctg ggc gcg aag atc gaa ctc tcc gat acg aag gct gcc tga			1584
Ala Gly Leu Gly Ala Lys Ile Glu Leu Ser Asp Thr Lys Ala Ala			
515	520	525	
tga			1587

<210> 75

<211> 33

<212> DNA

<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify DNA fragment having partial sequence of soybean PPO gene

<400> 75
cacaggaaag gtaccatggt ctgcatcgcc cag 33

<210> 76
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify DNA fragment having partial sequence of soybean PPO gene

<400> 76
cctgcagtc gagagtcct actatttgta cac 33

<210> 77
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PPO variant in which a region presumed to be FAD binding site of PPO

<220>
<221> unknown
<222> (1)...(6)
<223> any Xaa = any amino acid, unknown, or other

<400> 77
Gly Xaa Gly Xaa Xaa Gly
1 5

<210> 78
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PPO variant in which a region presumed to be FAD binding site of PPO

<400> 78
Gly Gly Gly Ile Ser Gly
1 5